



FEATURES		Source	Qualifiers
BASE COUNT	125	a	XhoI; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Best Local Similarity 64.2%; Pred. No. 2e-27; Length 454; Matches 201; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
ORIGIN	105	c	XbaI; The library was constructed by Dan Howe, University of Kentucky. cDNAs were synthesized from poly(A)+ RNA by oligo d(T) priming and directionally cloned into the Uni-ZAP XR lambda vector. The library was mass excised as phagemids and rescued in SOLR cells. The plasmid library was recovered from the SOLR cells and transformed in mass into DH10B cells for sequencing. <b>WARNING:</b> the library contains a small percentage of cDNAs derived from the bovine host cells.
BASE COUNT	125	a	XbaI; The library was harvested 3 weeks post inoculation with Glomus intraradices. <b>NOTE:</b> Vector: pBluescript SK; Site_1: EcoRI; Site_2: XbaI; M. truncatula sterilized seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoxies soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8 ). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using EXASIS helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France). <b>NOTE :</b> EST may be of fungal origin.
ORIGIN	105	c	XbaI; The library was harvested 3 weeks post inoculation with Glomus intraradices. <b>NOTE:</b> Vector: pBluescript SK; Site_1: EcoRI; Site_2: XbaI; M. truncatula sterilized seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoxies soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8 ). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using EXASIS helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France). <b>NOTE :</b> EST may be of fungal origin.
BASE COUNT	186	a	XbaI; The library was harvested 3 weeks post inoculation with Glomus intraradices. <b>NOTE:</b> Vector: pBluescript SK; Site_1: EcoRI; Site_2: XbaI; M. truncatula sterilized seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoxies soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8 ). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using EXASIS helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France). <b>NOTE :</b> EST may be of fungal origin.
RESULT	2		Query Match 32.8%; Score 133.8; DB 10; Length 489; Best Local Similarity 64.2%; Pred. No. 2e-27; Length 489; Matches 201; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
LOCUS	AL381742		EST 03-AUG-2000
DEFINITION	MtBC02F03		MTBC Medicago truncatula cDNA clone MtBC02F09 T3, mRNA sequence.
ACCESSION	AL381742		
VERSION	AL381742.1		GI: 9681493
RESULT	2		Query Match 32.8%; Score 133.8; DB 10; Length 489; Best Local Similarity 64.2%; Pred. No. 2e-27; Length 489; Matches 201; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
LOCUS	AL381742		EST 03-AUG-2000
DEFINITION	MtBC02F03		MTBC Medicago truncatula cDNA clone MtBC02F09 T3, mRNA sequence.
ACCESSION	AL381742		
VERSION	AL381742.1		GI: 9681493
RESULT	3		Query Match 32.8%; Score 133.8; DB 10; Length 489; Best Local Similarity 64.2%; Pred. No. 2e-27; Length 489; Matches 201; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
LOCUS	AQ963432		EST 03-AUG-2000
DEFINITION	AQ963432		MTBC Medicago truncatula cDNA clone MtBC02F09 T3, mRNA sequence.
ACCESSION	AQ963432		
VERSION	AQ963432.1		GI: 6791133
RESULT	3		Query Match 32.8%; Score 133.8; DB 10; Length 489; Best Local Similarity 64.2%; Pred. No. 2e-27; Length 489; Matches 201; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
LOCUS	AQ963432		EST 03-AUG-2000
DEFINITION	AQ963432		MTBC Medicago truncatula cDNA clone MtBC02F09 T3, mRNA sequence.
ACCESSION	AQ963432		
VERSION	AQ963432.1		GI: 6791133
REFERENCE	Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V., and Gamet, P.		
AUTHORS	Medicago truncatula ESTs from endomycorrhizal roots		
TITLE	Unpublished (2000)		
JOURNAL	Contact: Genoscope		
COMMENT	BP 191 91006 EVRY cedex - France		
Email:	seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		











Query Match	31.3%	Score	127.6	DB	10	; Length	389;
Best Local Similarity	63.9%	Pred.	No. 1.e-25;				
Matches	193;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	105	tccaaagtgtatcgctcgatcggaaagcgagaaggatacttcaagccatct	164				
Db	40	TCTAAAGATGTTAGTCCTCTGGACGTAAAGCGAAAGGCCATTTCGCTCCCTCT	99				
Qy	165	tccgttacacgaaatctatcgatggcgcccttgccaaaggactacgtacaatacgc	224				
Db	100	TGGTGGCGAGGAATATGAGTCGTCATTCACAGGACTTGAGCAATTAA	159				
Qy	225	gttcgttttttactatcgaaagagacggaaatcatatgttcgggggttcaag	284				
Db	160	ACTCGATCTATACCACTATGAGATGAGTCTATCTGGTACATTAA	219				
RESULT	13						
AA841097							
LOCUS	AA841097	349 bp	mRNA	EST	02-MAR-1998		
DEFINITION	MB3D6AA3E12n3	Brugia malayi day 6 post-infection third stage larvae					
ACCESSION	SAV96MLW-Bml3d6	Brugia malayi cDNA clone 3D6AA3E12 5', mRNA sequence.					
VERSION	AA841097						
KEYWORDS	EST.						
SOURCE	Brugia malayi.						
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.						
REFERENCE	1 (bases 1 to 349)						
AUTHORS	Blaxter M.L., Waterfall, M., Daub, J., Lizotte-Waniecki, M., Baron, L.						
JOURNAL							
TITLE	Genes expressed in day six post-infection, third stage larvae of Brugia malayi						
COMMENT	Unpublished (1997) Contact: Blaxter ML Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK.						
TEL:	+44 131 650 6760						
FAX:	+44 131 670 5450						
Email:	mark.blaxter@ed.ac.uk						
The ABI trace of this sequence can be viewed at <a href="http://www.sanger.ac.uk/brugia/3D6/MB3D6AA3E12r3.html">http://www.sanger.ac.uk/brugia/3D6/MB3D6AA3E12r3.html</a>							
Seq primer:	R3						
FEATURES	Location/Qualifiers						
source	1..349						
/organism="Brugia malayi"							
/strain="TRS Labs"							
/db_xref="txon:6279"							
/clone="3D6AA3E12"							
/clone_1lb="Brugia malayi day 6 post-infection third stage larvae SAV96MLW-Bml3d6"							
/sex="mixed"							
/dev_stage="third stage larvae, six days after infection"							
/lab_host="E. coli XII-Blue"							
/note="vector: lambdaZapII (Unizap XR); site_1: Eco R I (5' end); Site_2: Xba I (3' end); Brugia malayi is a							
RESULT	14						
AI490797							
LOCUS	AI490797	525 bp	mRNA	EST	18-MAY-2001		
DEFINITION	EST241505	tomato shoot, cornell Lycopersicon esculentum cDNA clone ESTB3G5 5', mRNA sequence.					
ACCESSION	AI490797						
VERSION	AI490797.1						
KEYWORDS	EST.						
SOURCE	tomato.						
ORGANISM	Lycopersicon esculentum						
	Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euanthids I; Solanales; Solanaceae; Solanum; Lycopersicon.						
REFERENCE	1 (bases 1 to 525)						
AUTHORS	Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nieman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Giovannoni, J.J.						
JOURNAL	van der Hoeven, R.S., Matern, A.L., Vision, T., Holt, I.E., Liang, F., and Tanksley, S.D. Generation of cDNA clones from tomato shoot meristem Unpublished (1998)						
COMMENT	Other PSTS: ESTR42282						
Contact: CUGI							
Clemson University Genomics Institute							
100 Jordan Hall, Clemson, SC 29634, USA							
Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>							
Seq primer:	M13 Reverse.						

FEATURES	5 prime sequence
source	Location/Qualifiers
I. . 525	1. . 527
/organism="Lycopersicon esculentum"	/organism="Lycopersicon esculentum"
/clone="taxon:4081"	/clone="taxon:4081"
/ab_xref="CLER366"	/ab_xref="CLER366"
/clone_1ib="Tomato shoot, Cornell"	/clone_1ib="Tomato shoot, Cornell"
/tissue_type="shoot meristem"	/tissue_type="shoot meristem"
/lab_host="XOLR"	/lab_host="XOLR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XbaI; EST Library: Oligo-dT Primed CDNA library made from tomato vegetative shoots including meristems and small expanding leaves."	/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XbaI; EST Library: Oligo-dT Primed CDNA library made from tomato vegetative shoots including meristems and small expanding leaves."
BASE COUNT	BASE COUNT
153 a 104 c 135 g 133 t	155 a 104 c 133 g 135 t
ORIGIN	ORIGIN
Query Match	Query Match
Best Local Similarity 31.0%	Best Local Similarity 31.0%
Matches 196; Conservative 0; Mismatches 116; Indels 0; Gaps 0;	Matches 196; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
Db 96 atggaaatccaaatccaaatgttttatcatcgatcgatcagaagaagcgtttccaa 155	Db 96 atggaaatccaaatccaaatgttttatcatcgatcgatcagaagaagcgtttccaa 155
Qy 18 ATGAAGTACATCCAGAATATCTCCCTCTCGGGAGAGCAGGAAAGCTCTTCACG 77	Qy 18 ATGAAGTACATCCAGAATATCTCCCTCTCGGGAGAGCAGGAAAGCTCTTCACG 77
Db 156 gccccatcttcgtacgacgaaatctatcgatcgatcggccatcgatcgatcg 215	Db 156 gccccatcttcgtacgacgaaatctatcgatcgatcggccatcgatcgatcg 215
Qy 78 GCGCTTCAGTGGCGGCCGATTAAATGAGGCGACCCATTGTCGAGTGTACGTTA 137	Qy 78 GCGCTTCAGTGGCGGCCGATTAAATGAGGCGACCCATTGTCGAGTGTACGTTA 137
Db 216 aaatacagccgttcttttacattatcgaaaggaaaggccgtatcgatcgatcg 275	Db 216 aaatacagccgttcttttacattatcgaaaggaaaggccgtatcgatcgatcg 275
Qy 138 AGTGTACACCTATGATCTATGCGGTGAGGAAGATGAGCAACTTCAGTTTGTCGTTG 197	Qy 138 AGTGTACACCTATGATCTATGCGGTGAGGAAGATGAGCAACTTCAGTTTGTCGTTG 197
Db 276 gtttcaagggtttagaaaggaaatgttgcgtatcgatcgatcgatcgatcg 335	Db 276 gtttcaagggtttagaaaggaaatgttgcgtatcgatcgatcgatcgatcg 335
Qy 198 ACTTACAAGGCCGTCAGGGAAAGTGTACCGTAAAGATAATGGGGATCCAC 257	Qy 198 ACTTACAAGGCCGTCAGGGAAAGTGTACCGTAAAGATAATGGGGATCCAC 257
Db 336 atccagagagtgccaggaaaaagcgatcgatcgatcgatcgatcgatcg 395	Db 336 atccagagagtgccaggaaaaagcgatcgatcgatcgatcgatcgatcg 395
Db 258 ATTCACGATTAACCAGAGAGAACGTCATCTGAGACGTTGTTCATCCT 317	Db 258 ATTCACGATTAACCAGAGAGAACGTCATCTGAGACGTTGTTCATCCT 317
Qy 396 tctaatgttgtt 407	Qy 396 tctaatgttgtt 407
Db 318 TCGAGGTTGTT 329	Db 318 TCGAGGTTGTT 329
RESULT 15	RESULT 15
A1772648	A1772648
LOCUS	AT77648
DEFINITION	527 bp mRNA
	BEST
ACCESSION	EST
A1772648	18-MAY-2001
VERSION	clone CLER3M12, mRNA sequence.
KEYWORDS	A1772648.1
EST	G1:5.270569
SOURCE	
ORGANISM	Lycopersicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS	D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, A.C.L., Niemi, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
TITLE	Generation of ESTs from <i>Pseudomonas</i> resistant tomato
JOURNAL	Unpublished (1999)
COMMENT	Contact: CUGI Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>
Search completed: March 2, 2002, 20:28:49	
Job time: 1519 sec	

Mon Mar 4 11:24:44 2002

us-09-540-235-1.rst

Page 10